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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/699,024

10/31/2003

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08/04/2009

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EXAMINER

WHALEY, PABLO S

ART UNIT

PAPER NUMBER

1631

MAIL DATE

DELIVERY MODE

08/04/2009

PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No. 10/699,024	Applicant(s) ABDEEN HUSSAN, JAGIR RAZAK JAINUL	
	Examiner PABLO WHALEY	Art Unit 1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 11 May 2009.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 3-6, 10 and 14-22 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 3-6, 10 and 14-22 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____ |

Art Unit: 1631

DETAILED ACTION

Status of Claims

Claims 3-6, 10, 14-22 are pending.

Claims 3-6, 10, 14-22 are rejected.

Claims 1-2, 7-9, 11-13, and 23 are cancelled.

Objections

The amended specification filed 05/11/2009 is acceptable. The objection to the specification is withdrawn.

Withdrawn Rejections

The rejection of claims 3-6, 10, 14-23 under 35 U.S.C. 101 is withdrawn in view of applicant's amendments, filed 05/11/2009.

The rejection of claims 4, 5, 10, and 14-23 under 35 U.S.C. 103(a) as being unpatentable over Taylor et al. (Computer and Chemistry, 1999, Vol. 23, p.365-385), in view of Schwartz et al. (Genome Research, 2000, Vol. 10, p.577-586) is withdrawn in view of applicant's amendments, filed 05/11/2009.

The rejection of claims 3-6, 10, and 14- 23 under 35 U.S.C. 103(a) as being unpatentable over Taylor et al. (Computer and Chemistry, 1999, Vol. 23, p.365-385), in view of Schwartz et al. (Genome Research, 2000, Vol. 10, p.577-586), as applied to claims 4, 5, 10, and 14-23 above, and further in view of Huysmans et al. (Proteins: Structure, Function, and Genetics, 1991, Vol. 11, p. 59-76) is withdrawn in view of applicant's amendments, filed 05/11/2009.

Claim rejections - 35 USC § 112, 1st Paragraph

Claims 3-6, 10, 14-22 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claims contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention.

Art Unit: 1631

This is a NEW MATTER rejection.

Claim 14 now recites step viii) the computer system generating or receiving a selection of one of the certain plurality of replets, wherein any non-selected one of the certain plurality of replets is deemed a redundant replet and the representing in step vii) is responsive to the selected one of the certain plurality of replets but not responsive to any redundant replete, ix) the computer system...receiving a selection of one of the replets deemed a redundant replete in step viii)." The previously examined claims recited the limitation "wherein redundant match set data structures corresponding to subsequences being matched by more than one replete are not generated." However this does not provide support for the newly added limitations. Applicant's response filed 05/11/2009 does not point to support for the newly recited limitations. No support has been found for these limitations in the specification, drawings, or claims of the application as originally filed. As the newly recited limitations are not supported by the originally filed claims or disclosure, the claims are rejected for reciting new matter. This rejection is necessitated by amendment.

Claim 14 now recites step ix) directed to a computer system generating or receiving one of the replets deemed a redundant replete in step viii). The previously examined claims recited the limitation "wherein redundant match set data structures corresponding to subsequences being matched by more than one replete are not generated." However this does not provide support for the newly added limitation, as the new limitation is directed to generating redundant replets. Applicant's response filed 05/11/2009 does not point to support for the newly recited limitations. No support has been found for these limitations in the specification, drawings, or claims of the application as originally filed. As the newly recited limitations are not supported by the originally filed claims or disclosure, the claims are rejected for reciting new matter. This rejection is necessitated by amendment.

Claim 14 now recites step x) directed to a computer system representing and presenting the sequence, wherein the representing in step x) is responsive to the one of the replets indicated by the

Art Unit: 1631

selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the representing in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the representing in step x) without repeating the generating of position parameters performed in step iii). Applicant's response filed 05/11/2009 does not point to support for the newly recited limitations. No support has been found for these limitations in the specification, drawings, or claims of the application as originally filed. As the newly recited limitations are not supported by the originally filed claims or disclosure, the claims are rejected for reciting new matter. This rejection is necessitated by amendment.

Claim rejections - 35 USC § 112, 2nd Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 3-6, 10, 14-22 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims that depend directly or indirectly from claim 14 are also rejected due to said dependence.

This rejection is necessitated by amendment.

Claim 14 now recites "vii) the computer system representing the sequence...and at least a portion of the stored match-set data,". It is unclear what limitation of the claimed method is intended, as this limitation merely refers to the previously recited computer system.

Claim 14 (steps vii and viii) now recites "wherein one of the subsequences is matched by a certain plurality of the replets and the method further includes: viii) the computer system generating or receiving a selection of one of the certain plurality of replets, wherein any non-selected one of the certain plurality of replets is deemed a redundant replet and the representing in step vii) is responsive to the

Art Unit: 1631

selected one of the certain plurality of replets but not responsive to any redundant replet.” It is unclear what actual steps are performed by the computer system and in what way these steps are “responsive” to non-selected replets, selected replets, and redundant replets.

Claim 14 (step x) now recites a computer system representing and presenting the sequence, wherein the representing in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the representing in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the representing in step x) without repeating the generating of position parameters performed in step iii). It is unclear what actual steps are performed by the computer system and in what way said representing is “responsive” to replets.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Art Unit: 1631

Claims 4, 5, and 14-22 are rejected under 35 U.S.C. 103(a) as being unpatentable over Taylor et al. (Computer and Chemistry, 1999, Vol. 23, p.365-385), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), and in view of Schwartz et al. (Genome Research, 2000, Vol. 10, p.577-586).

This rejection is necessitated by amendment.

Taylor teaches a computer implemented method and program for storing and presenting sequence data. In particular, the method requires specifying a set of probe sequences represented using code identifiers [Table 1], which equates to replets in view of the specification which exemplifies replets as patterns used to represent sequences [p.7]. Each probe sequence is compared to a database of sequences and match-sets are generated based on sequence identification, positional matches, and weights indicated degree of match (i.e. offset) [p.371-372, Section 4, p.374, Section 4.1.2, Fig. 3, and Fig. 4]. The iterative search and align cycle includes steps for removing similarity information [Fig. 3]. Gapped regions (i.e. mismatched) are replaced with an expression indicating the range of unmatched characters [p.368, Col. 1], which shows matched regions comprising "don't care" characters. Taylor teaches removing homologues (i.e. matching sequences) [p.370, Table 2, Fig. 5, Discussion]. Taylor shows a step for ordering of sequence information and connecting (i.e. concatenating) overlapping regions, and excluding redundant information from the backbone tree [p.369, Section 3.3.1, Fig. 2]. Taylor teaches constructing sequence matches for candidate template using a look-up table [Fig. 3]. The matching program represents sequences by reference to positional parameters and weight parameters [Fig. 4]. Additionally, Taylor shows a method for identifying multiple subsequences using one sequence code (i.e. replete) [Table 8, p.384, Col. 1]. Taylor shows segmenting matching sequences into parts to account for location-specific variations [Fig. 4, p.381-382, Section 6]. Talyor teaches an iterative search cycle wherein high scoring matches are combined with search templates [Fig. 3 and p.378, Col. 1, ¶2], which inherently shows adding new probes (i.e. replets) to a pre-existing set. Taylor also teaches recognition of repeats and identification of sub-families [p.384, Col. 1, ¶3].

Art Unit: 1631

Taylor does not teach offset information comprising first and second parameters denoting location in the sequence and offset from the location, as in claim 14.

Taylor does not specifically teach concatenating, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence, as in claim 14.

Taylor does not teach generating or receiving replets wherein non-selected replets are deemed redundant and the representing is responsive to selected replets but not responsive to redundant replets, as in claim 14 (step viii), or generating or receiving redundant replets, as in claim 14 (step ix).

Taylor does not teach a representing step responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the representing in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the representing in step x) without repeating the generating of position parameters performed in step iii), as in claim 14 (step x).

Taylor does not teach matching “don’t care” characters with a subsequence, as in claim 16.

Taylor does not specifically teach removing a replete from a pre-existing set, as in claim 22.

Chen teaches a program for identifying repeats in long DNA sequences [Introduction]. In particular, pattern identification programs are described for identifying positions within a sequence, identifying sequence repeats, and identifying location offsets [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1]. Uncoded information is discarded, and the remaining information (other than repeats) are concatenated then sent as input to another program [p.1698, Col. 1]. The program allows for encoding of repeat regions in the DNA sequences [p.1696-97, Methods]. This program is beneficial for improving search results through sequence compression [Introduction].

Schwartz teaches a computer-implemented method for presenting sequence data. In particular, Schwartz teaches the use of a program (RepeatMasker) that specifically generates repeat files based on

Art Unit: 1631

user submitted query files [p.578, Results, Col. 1 and Col. 2], and identifies redundant match-data structures in the query files being matched in order to prevent the generation of redundant data, as in claim 14. The RepeatMasker program generates masked sequence data (i.e. don't care data), searches masked sequences against databases, and merges search results to identify genes (i.e. backbone sequences) [p.580, Col. 2], as in claim 16. The method provide several options for generating and storing alignments (i.e. match-data structures) for each initial sequence file, including alignment coordinates, sequence position, and percent identity of gap-free segment information [p.578, Col. 2, Fig. 1], which shows generating sequence information, offset information. Multiple variations for storing matching subsequences is provided [Fig. 1, Fig. 2, Fig. 3, Fig. 4, Fig. 6]. Matched information is color coded and includes sequence information for exact matches and non-exact matches [p.580, Col. 2, ¶3, and Fig. 2], which corresponds to a "don't care character." Schwartz teaches concatenating data by chaining overlapping regions that appear in the same order and scoring of unmatched regions [p.582, Col. 2, ¶4, Fig. 6, p.585, Col. 1], as in claim 14. Schwartz teaches scoring parameters for mismatch, gap open, and gap extension used in alignment [Col. 585], which shows offset parameters.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by identifying offset information comprising first and second parameters denoting location in the sequence and offset from the location, as in claim 14, since Taylor shows match-sets generated based on sequence information, positional information, and degree of match (i.e. offset) [p.371-372, Section 4, p.374, Section 4.1.2, Fig. 3, and Fig. 4], and since Chen teaches pattern identification programs for identifying positions within a sequence, identifying sequence repeats, and identifying location offsets [p.1697, Col. 2, p.1698, Col. 1, and Fig. 1]. The motivation would have been to beneficially improve search results through sequence compression algorithms [Chen, Introduction].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by concatenating, in order, unmatched regions of sequences

Art Unit: 1631

that remain after deleting each matching subsequence to form and store a backbone sequence, as in claim 14, since Schwartz shows deleting duplicate regions based on chaining regions that appear in the same order and based on unmatched regions [p.582, Col. 2, ¶4, Fig. 6, p.585, Col. 1]. The motivation would have been to improve sequence matching using flexible and automated methods for avoiding duplicate matches when homologue regions appear in multiplicity, as suggested by Schwartz [p.583, Col. 2, ¶2].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by generating or receiving replets wherein non-selected replets are deemed redundant and the representing is responsive to selected replets but not responsive to redundant replets, as in claim 14 (step viii), or by generating or receiving redundant replets, as in claim 14 (step ix), since Chen shows methods for encoding of repeat regions in the DNA sequences [p.1696-97, Methods, Fig. 1], and since Schwartz shows methods for producing redundant matches and removing redundant alignments [p.580, Col. 2, Fig. 2, Fig. 6]. The motivation would have been to improve sequence matching by accommodating small overlaps between adjacent alignments [Schwartz, p.585, Col. 1, ¶3].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by representing sequences responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step viii) and wherein the computer system performs the representing in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the representing in step x) without repeating the generating of position parameters performed in step iii), as in claim 14 (step x), since Taylor provides a matching program that represents sequences by reference to positional and weight parameters [Fig. 4] and since Schwartz represents sequence based on positional parameters, length, and percent identity [Fig. 1]. The motivation would have been to identify sequence alignments using high-resolution displays, as suggested by Schwartz [Abstract].

Art Unit: 1631

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by matching “don’t care” characters with a subsequence, as in claim 16, since Schwartz provides multiple variations for identifying redundant matches and storing matching subsequences that includes sequence information for non-exact matches [p.580, Col. 2, Fig. 2, Fig. 6], which shows matching of “don’t care” information. The motivation would have been to use a program that can provide useful sequence comparisons even when sequences are not finished or have discontinuities, as suggested by Schwartz [p.581, Col. 1].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method of Taylor by removing a replet from a pre-existing set, as in claim 22, since Schwartz shows a step for comparing initial query files to repeat files to avoiding alignment repeats and uninformative information [p.578, Results]. The motivation would have been to improve sequence matching using flexible and automated methods for avoiding duplicate matches when homologue regions appear in multiplicity, as suggested by Schwartz [p.583, Col. 2, ¶2].

Claims 3-6, 10, and 14-22 are rejected under 35 U.S.C. 103(a) as being unpatentable over Taylor et al. (Computer and Chemistry, 1999, Vol. 23, p.365-385), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p.1696-1698), and in view of Schwartz et al. (Genome Research, 2000, Vol. 10, p.577-586), as applied to claims 4, 5, 10, and 14-23 above, and further in view of Huysmans et al. (Proteins: Structure, Function, and Genetics, 1991, Vol. 11, p. 59-76).

Taylor, Chen, and Schwartz make obvious a method for storing and presenting sequence data, as set forth above.

Taylor, Chen, and Schwartz do not teach storing information in a table using a “pointer”, as in claims 3 and 6.

Art Unit: 1631

Taylor, Chen, and Schwartz do not teach storing multiple views of the sequence data at multiple levels of abstraction, as in claim 10.

Huysmans teaches a relational database for storing sequence and position identifier data using relational pointers [Table I, Table II, Fig. 4, Fig. 5, p.65, Col. 1]. This method is beneficial for efficiently accessing and manipulating large amounts of information [p.67, Col. 1, p.74, Col. 1].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Taylor, Chen, and Schwartz by storing information in a table using a “pointer”, as in claims 3 and 6, since Huysmans teaches a relational database for storing sequence and position identifier data using relational pointers obtained from homology-based applications [Abstract, Table I, Table II, Fig. 4, Fig. 5, p.65, Col. 1]. The motivation would have been to incorporate functionality for efficiently accessing and manipulating large amounts of sequence and positional information, as suggested by Huysmans [p.67, Col. 1, p.74, Col. 1].

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the method made obvious by Taylor, Chen, and Schwartz by storing multiple views of the sequence data at multiple levels of abstraction, as in claim 10, since Schwartz shows multiple views for graphically presenting data [Fig. 1-5] and Huysmans shows storing sequence information at multiple levels of abstraction (e.g. micro and macro) [Fig. 1, Fig. 2]. The motivation would have been to provide users with the ability to compares genomic sequences using different types of information, as suggested by Schwartz [p.583, Col. 2, Discussion].

Response to Arguments

Applicant's arguments filed 05/11/2009 that the combination of Taylor, Schwartz, and Huysmans do not teach for each replet, a match-set data structure comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a

Art Unit: 1631

first and second position parameter, the first position parameter denoting a location in the sequence and the second position parameter denoting an offset from the location" have been fully considered but are moot in view of the new grounds of rejections.

Applicant's arguments filed 05/11/2009 that the combination of Taylor, Schwartz, and Huysmans do not teach multiple ways to represent a sequence depending upon which replet is chosen for representation have been fully considered but are moot in view of the new grounds of rejections.

Applicant's arguments filed 05/11/2009 that the combination of Taylor, Schwartz, and Huysmans do not teach allowing the user to choose among redundant reptlets for user control of output have been fully considered. In response, these features are not recited in the rejected claim(s). Although the claims are interpreted in light of the specification, limitations from the specification are not read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Art Unit: 1631

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Pablo Whaley whose telephone number is (571)272-4425. The examiner can normally be reached on 9:30am - 6pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran can be reached at 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Pablo S. Whaley

Patent Examiner

Art Unit 1631

/PW/

/SHUBO (Joe) ZHOU/

Primary Examiner, Art Unit 1631

Application/Control Number: 10/699,024

Page 14

Art Unit: 1631